

SEQUENCE LISTING

<110> Madeline M. Butler
Andrew T. Watt
Susan M. Freier
Jacqueline Wyatt

<120> ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION

<130> ISPH-0587

<160> 230

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<211> 20

<212> DNA

<213> Artificial Sequence

<220> .

<223> Antisense Oligonucleotide

<400> 1

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<223> Antisense Oligonucleotide

<400> 2

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<211> 3804

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (278)...(3508)

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ccttaaaaag gaagaccagt gatgctagga tggagtgaaa cccaagagga agtgccatca 180
tgaggaatca atgagagatc tgtgaagaga gagggctggg tgggagccca gaaggataga 240
acctggaaga tcaatatctc ccgtgagga aataaca atg gag cca ggt tct aag 295
Met Glu Pro Gly Ser Lys

1

5

tca gtg tct agg tca gac tgg caa cct gaa cca cac cag agg cct ata 343
Ser Val Ser Arg Ser Asp Trp Gln Pro Glu Pro His Gln Arg Pro Ile

10

15

20

SECRET

ctg ggc gtc cgt gcc gcc ttc ccc gag ggt ttc cac ccc cga cgc tcc	3127
Leu Gly Val Arg Ala Ala Phe Pro Glu Gly Phe His Pro Arg Arg Ser	
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agc cag ggt gcc aca cag atg ccc ctc tac tcc tca ccc ata gtc aag	3175
Ser Gln Gly Ala Thr Gln Met Pro Leu Tyr Ser Ser Pro Ile Val Lys	
955 960 965	
aac ccc ttc atg tcg ccg ctg ctg gca ccc gac agc atg ctc aag agc	3223
Asn Pro Phe Met Ser Pro Leu Leu Ala Pro Asp Ser Met Leu Lys Ser	
970 975 980	
ctg cca cct gtg cac atc gtg gcg tgc gcg ctg gac ccc atg ctg gac	3271
Leu Pro Pro Val His Ile Val Ala Cys Ala Leu Asp Pro Met Leu Asp	
985 990 995	
gac tcg gtc atg ctc gcg cgg cga ctg cgc aac ctg ggc cag ccg gtg	3319
Asp Ser Val Met Leu Ala Arg Arg Leu Arg Asn Leu Gly Gln Pro Val	
1000 1005 1010	
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Thr Leu Arg Val Val Glu Asp Leu Pro His Gly Phe Leu Thr Leu Ala	
1015 1020 1025 1030	
gcg ctg tgc cgc gag acg cgc cag gcc gca gag ctg tgc gtg gag cgc	3415
Ala Leu Cys Arg Glu Thr Arg Gln Ala Ala Glu Leu Cys Val Glu Arg	
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atc cgc ctc gtc ctc act cct ccc gcc gga gcc ggg ccg agc ggg gag	3463
Ile Arg Leu Val Leu Thr Pro Pro Ala Gly Ala Gly Pro Ser Gly Glu	
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Thr Gly Ala Ala Gly Val Asp Gly Gly Cys Gly Gly Arg His	
1065 1070 1075	
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gacctgcaag ccaccgctgc cttttgctgc tgctgctgcg gcgaccgccc cagggacggg	3748
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<221> CDS
 <222> (593)...(2872)

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ctcaggagat tggactccta gatccaggaa gaaggccaaa agacctggtc agtgggtttc 240
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tagaaagagg atgaggatgc agccgcaggc ttctagaaga caaggagata aattcctagg 360
tgtgagagag aagataatag gaaggccccct gcgtctccag gaggattggg acagacctga 420
ggaaggagag ggctcggctt tggactcctg catctcagca aggacgggtcc taggtttgaa 480
tacttggttg gcctagggaa agagaggaag ggcattggact cctgggcctg acagagcaaa 540
gggtaaccac agaccttccc atcttctcac agcctcagcg ttctcacaca gc atg gat 598
Met Asp

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1

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tta cgc acg atg aca cag tgc ctg gtg aca ctc gca gaa gac aat atg 646
Leu Arg Thr Met Thr Gln Ser Leu Val Thr Leu Ala Glu Asp Asn Met
5 10 15

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gcc ttc ttc tca agc cag ggc cca gga gag aca gca cgg cgg ctg tct 694
Ala Phe Phe Ser Ser Gln Gly Pro Gly Glu Thr Ala Arg Arg Leu Ser
20 25 30

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aat gtc ttt gca ggt gtt cgg gaa cag gca ctg ggg ctg gaa cca acc 742
Asn Val Phe Ala Gly Val Arg Glu Gln Ala Leu Gly Leu Glu Pro Thr
35 40 45 50

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cta ggc caa ctg ttg ggt gtg gca cac cat ttt gac ctg gac aca gag 790
Leu Gly Gln Leu Leu Gly Val Ala His His Phe Asp Leu Asp Thr Glu
55 60 65

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aca cca gcc aac gga tac cgt agt ttg gtg cac aca gcc cga tgc tgc 838
Thr Pro Ala Asn Gly Tyr Arg Ser Leu Val His Thr Ala Arg Cys Cys
70 75 80

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ctg gca cac cta cta cac aaa tcc cgc tat gtg gct tct aac cgc aaa 886
Leu Ala His Leu Leu His Lys Ser Arg Tyr Val Ala Ser Asn Arg Lys
85 90 95

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agt atc ttc ttc cgt gcc agc cac aac cta gca gag ctg gag gcc tac 934
Ser Ile Phe Phe Arg Ala Ser His Asn Leu Ala Glu Leu Glu Ala Tyr
100 105 110

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ctg gcc gcc ctc acc cag ctc cgt gct atg gcc tac tat gcc cag cgc 982
Leu Ala Ala Leu Thr Gln Leu Arg Ala Met Ala Tyr Tyr Ala Gln Arg
115 120 125 130

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ctg ctg acc atc aac cga cca gga gtg ctc ttc ttc gag ggt gat gaa 1030
Leu Leu Thr Ile Asn Arg Pro Gly Val Leu Phe Phe Glu Gly Asp Glu
135 140 145

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gga ctc acc gct gac ttc ctg caa gag tat gtc acg cta cac aaa ggc 1078
Gly Leu Thr Ala Asp Phe Leu Gln Glu Tyr Val Thr Leu His Lys Gly
150 155 160

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Leu	Ala	Gly	Asp	Ser	Ala	Gly	Gly	Asn	Leu	Cys	Ile	Thr	Val	Ser	Leu	
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cgg	gca	gca	gcc	tat	gga	gtg	agg	gtg	cca	gat	ggc	atc	atg	gca	gcc	1942
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Tyr	Pro	Val	Thr		Leu	Gln	Ser	Ser	Ala	Ser	Pro	Ser	Arg	Leu	Leu	
			455					460						465		
agc	ctc	atg	gac	cct	ctt	cta	cca	ctg	agc	gta	ctc	tct	aag	tgt	gtc	2038
Ser	Leu	Met	Asp	Pro	Leu	Leu	Pro	Leu	Ser	Val	Leu	Ser	Lys	Cys	Val	
			470					475					480			
agt	gcc	tat	tca	ggg	aca	gag	gca	gag	gac	cat	ttt	gac	tca	gac	cag	2086
Ser	Ala	Tyr	Ser	Gly	Thr	Glu	Ala	Glu	Asp	His	Phe	Asp	Ser	Asp	Gln	
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aag	gca	cta	ggc	gtg	atg	ggg	ctg	gtg	cag	aga	gac	act	tcg	ctg	ttc	2134
Lys	Ala	Leu	Gly	Val	Met	Gly	Leu	Val	Gln	Arg	Asp	Thr	Ser	Leu	Phe	
	500					505					510					
ctc	aga	gac	ctc	cga	ctg	ggg	gcc	tcc	tca	tgg	ctc	aac	tcc	ttc	ccg	2182
Leu	Arg	Asp	Leu	Arg	Leu	Gly	Ala	Ser	Ser	Trp	Leu	Asn	Ser	Phe	Pro	
515					520					525					530	
gaa	cta	agt	gga	cgc	aag	ccc	caa	aag	acc	aca	tcg	ccc	aca	gca	gag	2230
Glu	Leu	Ser	Gly	Arg	Lys	Pro	Gln	Lys	Thr	Thr	Ser	Pro	Thr	Ala	Glu	
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tct	gtg	cgc	ccc	acg	gag	tct	atg	cgc	agg	agt	gtg	tct	gag	gca	gcc	2278
Ser	Val	Arg	Pro	Thr	Glu	Ser	Met	Arg	Arg	Ser	Val	Ser	Glu	Ala	Ala	
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Leu	Ala	Gln	Pro	Glu	Gly	Leu	Leu	Gly	Thr	Asp	Thr	Leu	Lys	Lys	Leu	
		565				570						575				
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Thr	Ile	Lys	Asp	Leu	Ser	Asn	Ser	Glu	Pro	Ser	Asp	Ser	Pro	Glu	Met	
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tca	cag	tca	atg	gag	aca	ctt	ggc	ccc	tcc	aca	ccc	tct	gat	gtc	aac	2422
Ser	Gln	Ser	Met	Glu	Thr	Leu	Gly	Pro	Ser	Thr	Pro	Ser	Asp	Val	Asn	
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Phe	Phe	Leu	Arg	Pro	Gly	Asn	Ser	Gln	Glu	Glu	Ala	Glu	Ala	Lys	Asp	

gaa gtg aga ccc atg gac gga gtc ccc cgc gtg cgc gct gct ttc cct	2518
Glu Val Arg Pro Met Asp Gly Val Pro Arg Val Arg Ala Ala Phe Pro	
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Glu Gly Phe His Pro Arg Arg Ser Ser Gln Gly Val Leu His Met Pro	
645 650 655	
ctc tac acg tca ccc ata gtc aag aac ccc ttc atg tct cct ctg ctg	2614
Leu Tyr Thr Ser Pro Ile Val Lys Asn Pro Phe Met Ser Pro Leu Leu	
660 665 670	
gcc cct gac agc atg ctg aag acc ttg ccg cct gtg cac ctt gtg gct	2662
Ala Pro Asp Ser Met Leu Lys Thr Leu Pro Pro Val His Leu Val Ala	
675 680 685 690	
tgc gct ctg gac ccc atg cta gat gac tgc gtc atg ttc gcg cgg cga	2710
Cys Ala Leu Asp Pro Met Leu Asp Asp Ser Val Met Phe Ala Arg Arg	
695 700 705	
ctg cgc gac ctg ggc cag ccg gtg acg ctg aaa gtg gta gaa gat ctg	2758
Leu Arg Asp Leu Gly Gln Pro Val Thr Leu Lys Val Val Glu Asp Leu	
710 715 720	
ccg cat ggc ttc ctg agc ctg gcg gca ctg tgt cgc gag acc cgg cag	2806
Pro His Gly Phe Leu Ser Leu Ala Ala Leu Cys Arg Glu Thr Arg Gln	
725 730 735	
gcc acg gag ttc tgc gtg cag cgc atc cgg ctg atc ctc acc ccg cct	2854
Ala Thr Glu Phe Cys Val Gln Arg Ile Arg Leu Ile Leu Thr Pro Pro	
740 745 750	
gct gca cca ctg aac tga gctggggacg gcggggggcg gcactaaaag	2902
Ala Ala Pro Leu Asn	
755	
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 cctgcccaca gcctcaaggc tcattccaaa c atg gac ctg cgc aca atg aca 652
 Met Asp Leu Arg Thr Met Thr
 1 5

cag tcg ctg gtg act ctg gcg gag gac aac ata gcc ttc ttc tcg agc 700
 Gln Ser Leu Val Thr Leu Ala Glu Asp Asn Ile Ala Phe Phe Ser Ser
 10 15 20

cag ggt cct ggg gaa acg gcc cag cgg ctg tca ggc gtt ttt gcc ggt 748
 Gln Gly Pro Gly Glu Thr Ala Gln Arg Leu Ser Gly Val Phe Ala Gly
 25 30 35

gta cgg gag cag gcg ctg ggg ctg gag ccg gcc ctg ggc cgc ctg ctg 796
 Val Arg Glu Gln Ala Leu Gly Leu Glu Pro Ala Leu Gly Arg Leu Leu
 40 45 50 55

ggg gtg gcg cac ctc ttt gac ctg gac cca gag aca ccg gcc aac ggg 844
 Gly Val Ala His Leu Phe Asp Leu Asp Pro Glu Thr Pro Ala Asn Gly
 60 65 70

tac cgc agc cta gtg cac aca gcc cgc tgc tgc ctg gcg cac ctc ctg 892
 Tyr Arg Ser Leu Val His Thr Ala Arg Cys Cys Leu Ala His Leu Leu
 75 80 85

cac aaa tcc cgc tat gtg gcc tcc aac cgc cgc agc atc ttc ttc cgc 940
 His Lys Ser Arg Tyr Val Ala Ser Asn Arg Arg Ser Ile Phe Phe Arg
 90 95 100

acc agc cac aac ctg gcc gag ctg gag gcc tac ctg gct gcc ctc acc 988
 Thr Ser His Asn Leu Ala Glu Leu Glu Ala Tyr Leu Ala Ala Leu Thr
 105 110 115

cag ctc cgc gct ctg gtc tac tac gcc cag cgc ctg ctg gtt acc aat 1036
 Gln Leu Arg Ala Leu Val Tyr Tyr Ala Gln Arg Leu Leu Val Thr Asn
 120 125 130 135

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 Arg Pro Gly Val Leu Phe Phe Glu Gly Asp Glu Gly Leu Thr Ala Asp
 140 145 150

ttc ctc cgg gag tat gtc acg ctg cat aag gga tgc ttc tat ggc cgc 1132

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Cys	Leu	Gly	Phe	Gln	Phe	Thr	Pro	Ala	Ile	Arg	Pro	Phe	Leu	Gln	Thr	
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	185					190					195					
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Ala	Ile	Asp	Pro	Glu	Leu	Arg	Gly	Ala	Glu	Phe	Glu	Arg	Ile	Thr	Gln	
				220					225					230		
aac	ctg	gac	gtg	cac	ttc	tgg	aaa	gcc	ttc	tgg	aac	atc	acc	gag	atg	1372
Asn	Leu	Asp	Val	His	Phe	Trp	Lys	Ala	Phe	Trp	Asn	Ile	Thr	Glu	Met	
			235					240					245			
gaa	gtg	cta	tcg	tct	ctg	gcc	aac	atg	gca	tcg	gcc	acc	gtg	agg	gta	1420
Glu	Val	Leu	Ser	Ser	Leu	Ala	Asn	Met	Ala	Ser	Ala	Thr	Val	Arg	Val	
		250					255					260				
agc	cgc	ctg	ctc	agc	ctg	cca	ccc	gaa	gcc	ttt	gag	atg	cca	ctg	act	1468
Ser	Arg	Leu	Leu	Ser	Leu	Pro	Pro	Glu	Ala	Phe	Glu	Met	Pro	Leu	Thr	
	265					270					275					
gcc	gac	ccc	acg	ctc	acg	gtc	acc	atc	tca	ccc	cca	ctg	gcc	cac	aca	1516
Ala	Asp	Pro	Thr	Leu	Thr	Val	Thr	Ile	Ser	Pro	Pro	Leu	Ala	His	Thr	
280					285					290					295	
ggc	cct	ggg	ccc	gtc	ctc	gtc	agg	ctc	atc	tcc	tat	gac	ctg	cgt	gaa	1564
Gly	Pro	Gly	Pro	Val	Leu	Val	Arg	Leu	Ile	Ser	Tyr	Asp	Leu	Arg	Glu	
				300					305					310		
gga	cag	gac	agt	gag	gag	ctc	agc	agc	ctg	ata	aag	tcc	aac	ggc	caa	1612
Gly	Gln	Asp	Ser	Glu	Glu	Leu	Ser	Ser	Leu	Ile	Lys	Ser	Asn	Gly	Gln	
			315					320					325			
cgg	agc	ctg	gag	ctg	tgg	ccg	cgc	ccc	cag	cag	gca	ccc	cgc	tcg	cgg	1660
Arg	Ser	Leu	Glu	Leu	Trp	Pro	Arg	Pro	Gln	Gln	Ala	Pro	Arg	Ser	Arg	
		330					335					340				
tcc	ctg	ata	gtg	cac	ttc	cac	ggc	ggg	ggc	ttt	gtg	gcc	cag	acc	tcc	1708
Ser	Leu	Ile	Val	His	Phe	His	Gly	Gly	Gly	Phe	Val	Ala	Gln	Thr	Ser	
	345					350					355					
aga	tcc	cac	gag	ccc	tac	ctc	aag	agc	tgg	gcc	cag	gag	ctg	ggc	gcc	1756
Arg	Ser	His	Glu	Pro	Tyr	Leu	Lys	Ser	Trp	Ala	Gln	Glu	Leu	Gly	Ala	
360					365				370						375	
ccc	atc	atc	tcc	atc	gac	tac	tcc	ctg	gcc	cct	gag	gcc	ccc	ttc	ccc	1804
Pro	Ile	Ile	Ser	Ile	Asp	Tyr	Ser	Leu	Ala	Pro	Glu	Ala	Pro	Phe	Pro	

380										385					390					
cgt	gcg	ctg	gag	gag	tgc	ttc	ttc	gcc	tac	tgc	tgg	gcc	atc	aag	cac	1852				
Arg	Ala	Leu	Glu	Glu	Cys	Phe	Phe	Ala	Tyr	Cys	Trp	Ala	Ile	Lys	His					
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Cys	Ala	Leu	Leu	Gly	Ser	Thr	Gly	Glu	Arg	Ile	Cys	Leu	Ala	Gly	Asp					
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agt	gca	ggc	ggg	aac	ctc	tgc	ttc	acc	gtg	gct	ctt	cgg	gca	gca	gcc	1948				
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